

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
- (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
- (iii) NUMBER OF SEQUENCES: 111
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 - (B) STREET: 1100 NORTH GLEBE ROAD
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 22201-4714
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/612,973
 - (B) FILING DATE: 11-MAR-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BYRNE, THOMAS E.
 - (B) REGISTRATION NUMBER: 32,205
 - (C) REFERENCE/DOCKET NUMBER: 1487-10
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT
AACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA

144

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala			
35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG			192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT			240
Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG			288
Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu			
85	90	95	
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC			336
Leu Val Gly Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu			
100	105	110	
GCG GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC			384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg			
115	120	125	
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC			432
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
130	135	140	
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT			480
Phe Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro			
145	150	155	160
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC			528
Thr Ala Leu Val Val Ser Gln Leu Arg Ile Pro Gln Ala Val			
165	170	175	
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC			576
Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala			
180	185	190	
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA			624
Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu			
195	200	205	
CTC TTT GCT CTC TAATAG			642
Leu Phe Ala Leu			
210			

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys			
1	5	10	15

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
 20 25 30

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
 35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
 50 55 60

Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
 65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu
 85 90 95

Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu
 100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg
 115 120 125

Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His
 130 135 140

Phe Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
 145 150 155 160

Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val
 165 170 175

Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala
 180 185 190

Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu
 195 200 205

Leu Phe Ala Leu
 210

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
A GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
C TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
T GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
A GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
G CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	

CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768
Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile	
245 250 255	
GTG ATG CTA CTC TTT GCT CCC TAATAG	795
Val Met Leu Leu Phe Ala Pro	
260	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 210 215 220
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala
 225 230 235 240
 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile
 245 250 255
 Val Met Leu Leu Phe Ala Pro
 260

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..630
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGT GCT GCC AGA	96
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95	288
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110	336
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125	384
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His 130 135 140	432
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 145 150 155 160	480
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile 165 170 175	528
CG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr 180 185 190	576
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn 195 200 205	624
GG TAATAG Trp 210	633

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

- Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

T
R
P
H
C
D
S

INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

. (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..480

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	

CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
---	----

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val			
20	25	30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA		144	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala			
35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG		192	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC		240	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG		288	
Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu			
85	90	95	
GTC GTT GGG GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC		336	
Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu			
100	105	110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC		384	
Gys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg			
115	120	125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT		432	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
130	135	140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG		483	
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser			
145	150	155	160

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys			
1	5	10	15
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val			
20	25	30	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala			
35	40	45	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80

Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu
 85 90 95
 Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu
 100 105 110
 Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 115 120 125
 Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His
 130 135 140
 Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..477
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	

AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288	
Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu		
85	90	95
CTC GTT GGG GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336	
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu		
100	105	110
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384	
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg		
115	120	125
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His		
130	135	140
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG AAC TGG TAATAG	480	
Val Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp		
145	150	155

INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val
20 25 30

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu

50 55 60
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala

65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu
 . 85 90 95

Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu
100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
115 120 125

Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His
120 125 130 135 140

Val-Ser-Glu-His-Arc-Met-Ala-Trp-Asp-Met-Met-Met-Asp-Trp

145 **150** **155**

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..633

 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	CTG	GGT	AAG	GCC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
					5				10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
					20				25					30		
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
					35				40				45			
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
					50			55				60				
CTG	TCC	TGT	CTA	ACC	ATT	CCA	GCT	TCC	GCT	TAC	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
					65			70			75			80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
					85				90				95			
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
					100				105				110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
					115			120				125				
CTC	GCG	GCT	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACA	ACA	ATA	CGA	CGC	CAC	432

Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His			
130	135	140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG		480	
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val			
145	150	155	160
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC		528	
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile			
165	170	175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT		576	
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr			
180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC		624	
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Ile Arg Arg His

130 135 140
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
195 200 205

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCACTGA TACCCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCA G TTTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC
 Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15

48

GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

96

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA
 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
 35 40 45

144

ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG
 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60

192

CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80

240

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95	288
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110	336
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125	384
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His 130 135 140	432
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145 150 155 160	480
GAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 165 170 175	528
ATG GCT TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 185 190	576
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala 195 200 205	624
GCG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val 210 215 220	672
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro 225 230 235 240	723

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175
Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
180 185 190
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala
195 200 205
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val
210 215 220
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro
225 230 235

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..558

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	48
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	96
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	144
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	192
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	240
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	288
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	336
100 105 110	
CTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	384
115 120 125	
GTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	432
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	480
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	528
165 170 175	
ATG GCT TGG GAT ATG ATG AAC TGG TAATAG Met Ala Trp Asp Met Met Asn Trp	561
180 185	

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

1	5	10	15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg				
	20	25	30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala				
	35	40	45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu				
	50	55	60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val				
	65	70	75	80
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val				
	85	90	95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys				
	100	105	110	
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr				
	115	120	125	
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His				
	130	135	140	
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val				
	145	150	155	160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg				
	165	170	175	
Met Ala Trp Asp Met Met Met Asn Trp				
	180	185		

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..603

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	48
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	96
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	144
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	192
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	240
65 70 75 80	
TGC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	288
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	336
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	384
115 120 125	
GTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	432
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	480
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	528
165 170 175	
ATG GCT TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	576
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG Val Ser Gln Leu Leu Arg Ile Leu	606
195 200	

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
180 185 190

Val Ser Gln Leu Leu Arg Ile Leu
195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
TG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Ceu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC GTG ATC GAG GGC AGA CAC CAT CAC CAC	624
Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His	
195 200 205	
CAT CAC TAATAG	636
His His	

210

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
180 185 190

Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His
195 200 205

His His
210

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAC ATC CCG CTC GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC	96
Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala	
20 25 30	
GTT GCG CAT GGC GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA	144
Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr	
35 40 45	
GGG AAT TTG CCC GGT TGC TCC TTT TCT ATT TTC CTT CTC GCT CTG TTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe	
50 55 60	
TCT TGC TTA ATT CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT	240
Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser	
65 70 75 80	
GGC CTC TAT GTC CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC	288
Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCC GAT GAC GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC	336
Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val	
100 105 110	
CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG	384
Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val	
115 120 125	
GCA GTC AAG TAC GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG	432
Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val	
130 135 140	
GAC CTA TTA GTG GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT	480
Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly	
145 150 155 160	

GAC ATG TGT GGG GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg 165 170 175	528
CCT CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro 180 185 190	576
GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT ATG ATG ATG AAC TGG Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 195 200 205	624
TAATAG	634

2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
20 25 30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
50 55 60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
65 70 75 80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
85 90 95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
100 105 110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
115 120 125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
130 135 140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
145 150 155 160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
165 170 175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp
195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG 48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
1 5 10 15

GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT 96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
20 25 30

CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA 144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
35 40 45

GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC 192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
50 55 60

TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT 240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
65 70 75 80

GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT 288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
85 90 95

GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC 336

Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val			
100	105	110	
ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG			384
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu			
115	120	125	
TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT			432
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val			
130	135	140	
GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA			480
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly			
145	150	155	160
GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG			528
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg			
165	170	175	
CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT			576
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser			
180	185	190	
GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG			624
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp			
195	200	205	
TAATAG			630

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met
1				5			10							15	

Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala
					20			25				30			

Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr
					35		40				45				

Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
					50		55		60						

Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser
					65		70		75		80				

Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr
					85			90			95				

Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
100 105 110

Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
115 120 125

Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
130 135 140

Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
145 150 155 160

Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
165 170 175

Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
180 185 190

Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
195 200 205

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1473

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG	48
Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser	
1 5 10 15	
GAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC	96
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala	
20 25 30	
CAT TGG GGA GTC CTG GCG CTC GCC TAC TAT TCC ATG GTG GGG AAC	144
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn	
35 40 45	
TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG	192
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly	
50 55 60	
CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT	240
His Thr Arg Val Ser Gly Gly Ala Ala Ser Asp Thr Arg Gly Leu	
65 70 75 80	
GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC	288
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn	
85 90 95	
ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC	336
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp	
100 105 110	
TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC	384
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe	
115 120 125	
AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC	432

Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp			
130	135	140	
AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC			480
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser			
145	150	155	160
TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT			528
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly			
165	170	175	
ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG			576
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro			
180	185	190	
AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT			624
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr			
195	200	205	
AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG			672
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg			
210	215	220	
CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG			720
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly			
225	230	235	240
TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC			768
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly			
245	250	255	
AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG			816
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu			
260	265	270	
GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT			864
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys			
275	280	285	
ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC			912
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn			
290	295	300	
TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG			960
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg			
305	310	315	320
TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG			1008
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu			
325	330	335	
GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG			1056
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu			
340	345	350	
TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC			1104
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr			
355	360	365	
GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC			1152
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr			
370	375	380	

GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC		1200
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val		
385 390 395 400		
CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA		1248
Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu		
405 410 415		
TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG		1296
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu		
420 425 430		
GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC		1344
Val Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser		
435 440 445		
TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC		1392
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val		
450 455 460		
CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT		1440
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu		
465 470 475 480		
CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA		1476
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala		
485 490		

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser		
1 5 10 15		
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala		
20 25 30		
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn		
35 40 45		
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly		
50 55 60		
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu		
65 70 75 80		
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn		
85 90 95		
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp		
100 105 110		

Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
115 120 125

Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
130 135 140

Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
145 150 155 160

Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
165 170 175

Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
180 185 190

Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
195 200 205

Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
210 215 220

Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
225 230 235 240

Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
245 250 255

Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
260 265 270

Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys
275 280 285

Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn
290 295 300

Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg
305 310 315 320

Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu
325 330 335

Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu
340 345 350

Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr
355 360 365

Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr
370 375 380

Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val
385 390 395 400

Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu
405 410 415

Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu
420 425 430

Val Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser

435

440

445

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val
 450 455 460

Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu
 465 470 475 480

Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 485 490

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

D
G
N
Y
D
E
M
G
C
G
C
T

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	46
1 5 10 15	

GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	94
20 25 30	

GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	142
35 40 45	

GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	190
50 55 60	

TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	238
65 70 75	

AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	286
80 85 90 95	

ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	334
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	382
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	430
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	478
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	526
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	574
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	622
195 200 205	
GCG AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	670
210 215 220	
TGT GGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	718
225 230 235	
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr	766
240 245 250 255	
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His	814
260 265 270	
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile	862
275 280 285	
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala	910
290 295 300	
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp	958
305 310 315	
AGA TCA GAG CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG CAG AGT Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ser	1006
320 325 330 335	
GGC AGA GCT TAATTA	1021

Gly Arg Ala

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val
1 5 10 15

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
20 25 30

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val
35 40 45

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe
50 55 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser
65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
100 105 110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
165 170 175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly
325 330 335

Arg Ala

Q) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1032

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA 46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly
1 5 10 15

GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG 94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys
20 25 30

GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC 142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg
35 40 45

GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC 190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu
50 55 60

TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly 65 70 75	238
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln 80 85 90 95	286
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser 100 105 110	334
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala 115 120 125	382
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln 130 135 140	430
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro 145 150 155	478
GGG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val 160 165 170 175	526
G TG G TG G GG A CG A CC G AT CGG T TT G GT G TC CCC A CG T AT AAC T GG G GG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly 180 185 190	574
GGG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg 195 200 205	622
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220	670
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235	718
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255	766
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270	814
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285	862
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300	910
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp	958

305

310

315

AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG
 Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly
 320 325 330 335

1006

CAG ACA CCA TCA CCA TCA CTA AT AG
 Gln Thr Pro Ser Pro Pro Ser Leu
 340

1034

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val
 1 5 10 15

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 20 25 30

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val
 35 40 45

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe
 50 55 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser
 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
 85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
 100 105 110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln
325 330 335

Thr Pro Ser Pro Pro Ser Leu
340

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..942

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala
1 5 10 15

48

GGA GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp
20 25 30

96

ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC		144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile		
35 40 45		
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG		192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu		
50 55 60		
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC		240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ala Ala Leu Phe Tyr		
65 70 75 80		
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT		288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys		
85 90 95		
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT		336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr		
100 105 110		
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT		384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro		
115 120 125		
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT		432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr		
130 135 140		
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT		480
Gly Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly		
145 150 155 160		
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC		528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu		
165 170 175		
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG		576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met		
180 185 190		
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC		624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile		
195 200 205		
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG		672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg		
210 215 220		
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG		720
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu		
225 230 235 240		
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC		768
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro		
245 250 255		
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC		816
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly		
260 265 270		
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT		864

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
275 280 285

TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
290 295 300

TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG
Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
305 310

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala
1 5 10 15

Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp
20 25 30

Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile
35 40 45

Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu
50 55 60

Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr
65 70 75 80

Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys
85 90 95

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
100 105 110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
115 120 125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
130 135 140

Cys Phe Thr Pro Ser Pro Val Val Gly Thr Thr Asp Arg Phe Gly
145 150 155 160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
165 170 175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
180 185 190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Pro Pro Cys Asn Ile
195 200 205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
210 215 220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
225 230 235 240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
245 250 255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
260 265 270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
275 280 285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
290 295 300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
305 310

42) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC 48
Met Val Gly Asn Trp Ala Lys Val Leu Val Met Leu Leu Phe Ala
1 5 10 15

GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT 96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp
20 25 30

ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC 144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile
35 40 45

CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG 192

Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu			
50	55	60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC			240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr			
65	70	75	80
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT			288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys			
85	90	95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT			336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr			
100	105	110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT			384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro			
115	120	125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT			432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr			
130	135	140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT			480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly			
145	150	155	160
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC			528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu			
165	170	175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG			576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met			
180	185	190	
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC			624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile			
195	200	205	
GGG GGG GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG			672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg			
210	215	220	
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG			720
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu			
225	230	235	240
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC			768
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro			
245	250	255	
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC			816
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly			
260	265	270	
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT			864
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg			
275	280	285	
TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG			912
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu			

290

295

300

TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA CCA TCA CTA A
 Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu
 305 310 315
 TAG

958

961

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala
 1 5 10 15
 Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp
 20 25 30
 Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile
 35 40 45
 Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu
 50 55 60
 Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr
 65 70 75 80
 Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys
 85 90 95
 Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
 100 105 110
 Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
 115 120 125
 Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
 130 135 140
 Cys Phe Thr Pro Ser Pro Val Val Gly Thr Thr Asp Arg Phe Gly
 145 150 155 160
 Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
 165 170 175
 Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
 180 185 190
 Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
 195 200 205
 Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
 210 215 220
 Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu

225	230	235	240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro			
245		250	255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly			
260		265	270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg			
275		280	285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu			
290		295	300
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu			
305	310	315	

2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1392
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT	48
Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr	
1 5 10 15	
TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT	96
Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe	
20 25 30	
GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC	144
Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser	
35 40 45	
GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA	192
Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys	
50 55 60	
ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC	240
Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala	
65 70 75 80	

CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe 85 90 95	288
TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser 100 105 110	336
TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr 115 120 125	384
ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala 130 135 140	432
CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val 145 150 155 160	480
TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe 165 170 175	528
GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile 180 185 190	576
CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp 195 200 205	624
ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn 210 215 220	672
ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe 225 230 235 240	720
CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp 245 250 255	768
CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr 260 265 270	816
CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly 275 280 285	864
GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu 290 295 300	912
CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu 305 310 315 320	960
CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG	1008

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu			
325	330	335	
CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC		1056	
Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp			
340	345	350	
GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC		1104	
Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile			
355	360	365	
AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC		1152	
Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg			
370	375	380	
ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC		1200	
Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala			
385	390	395	400
GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG		1248	
Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala			
405	410	415	
GAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC		1296	
His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile			
420	425	430	
AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG		1344	
Eys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp			
435	440	445	
CTG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA		1395	
Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala			
450	455	460	

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr			
1	5	10	15
Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe			
20	25	30	
Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser			
35	40	45	
Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys			
50	55	60	
Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala			
65	70	75	80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe
85 90 95

Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser
100 105 110

Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr
115 120 125

Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala
130 135 140

Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val
145 150 155 160

Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe
165 170 175

Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile
180 185 190

Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp
195 200 205

Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
210 215 220

Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe
225 230 235 240

Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp
245 250 255

Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr
260 265 270

Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly
275 280 285

Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu
290 295 300

Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu
305 310 315 320

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu
325 330 335

Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp
340 345 350

Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile
355 360 365

Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg
370 375 380

Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala
385 390 395 400

Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala

405

410

415

His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile
 420 425 430

Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp
 435 440 445

Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	

GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	

ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	

CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	

TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110	336
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125	384
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His 130 135 140	432
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 145 150 155 160	480
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile 165 170 175	528
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr 180 185 190	576
GCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn 195 200 205	624
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 210 215 220	672
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala 225 230 235 240	720
GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val 245 250 255	768
GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly 260 265 270	816
GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro 275 280 285	864
GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 290 295 300	912
ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 305 310 315 320	960
TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro 325 330 335	1008
GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG	1056

Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp			
340	345	350	
GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC		1104	
Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr			
355	360	365	
TGC TGG CAC TAC GCG CCT CGA CCG TGT ATT GTA CCC GCG TCT CAG		1152	
Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln			
370	375	380	
GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG		1200	
Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly			
385	390	395	400
ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC		1248	
Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp			
405	410	415	
CG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG		1296	
Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp			
420	425	430	
GC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG		1344	
Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly			
435	440	445	
GCG CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC		1392	
Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys			
450	455	460	
CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC		1440	
Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys			
465	470	475	480
GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT		1488	
Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr			
485	490	495	
AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT		1536	
Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val			
500	505	510	
AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT		1584	
Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn			
515	520	525	
TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG		1632	
Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu			
530	535	540	
CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT		1680	
Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys			
545	550	555	560
TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT		1728	
Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His			
565	570	575	
CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT		1776	
Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val			
580	585	590	

GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu 595 600 605	1824
CTG GCA GAC GCG CGC ATC TGC GCC TTA TGG ATG ATG CTG CTG ATA Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile 610 615 620	1872
GCT CAA GCT GAG GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala 625 630 635 640	1920
GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys 645 650 655	1968
GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala 660 665 670	2016
TAC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro 675 680 685	2064
GGA GCT TAT GCC TAGTAA Arg Ala Tyr Ala 690	2082

Q) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 692 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu '1 5 10 15
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala
225 230 235 240

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
245 250 255

Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly
260 265 270

Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro
275 280 285

Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His
290 295 300

Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe
305 310 315 320

Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro
325 330 335

Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp
340 345 350

Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr
355 360 365

Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln
370 375 380

Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly
385 390 395 400

Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp
405 410 415

Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp
420 425 430

Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly

435

440

445

Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys
 450 455 460

Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys
 465 470 475 480

Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr
 485 490 495

Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val
 500 505 510

Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn
 515 520 525

Tyr Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu
 530 535 540

Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys
 545 550 555 560

Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His
 565 570 575

Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val
 580 585 590

Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu
 595 600 605

Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile
 610 615 620

Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala
 625 630 635 640

Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys
 645 650 655

Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala
 660 665 670

Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro
 675 680 685

Arg Ala Tyr Ala
 690

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2430

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
Q1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG	240
Phe Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA	432
Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC	480
Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	
GGC GTG AAC TAT GCA ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC	528
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile	
165 170 175	
TTC CTC TTG GCT TTG CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT	576
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr	

180	185	190	
GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser			624
195	200	205	
AAC TCA AGC ATT GTG TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro			672
210	215	220	
GGG TGC GTG CCC TGC GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val			720
225	230	235	240
GCG CTC ACC CCC ACG CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr			768
245	250	255	
A ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys			816
260	265	270	
T GCT ATG TAC GTG GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser			864
275	280	285	
C CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys			912
290	295	300	
A AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp			960
305	310	315	320
H ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln			1008
325	330	335	
CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His			1056
340	345	350	
TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp			1104
355	360	365	
GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His			1152
370	375	380	
ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val			1200
385	390	395	400
TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr			1248
405	410	415	
AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser			1296
420	425	430	

CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn 435 440 445	1344
TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys 450 455 460	1392
TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser 465 470 475 480	1440
GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile 485 490 495	1488
CTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser 500 505 510	1536
CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn 515 520 525	1584
TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro 530 535 540	1632
CGC CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe 545 550 555 560	1680
ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn 565 570 575	1728
AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 590	1776
ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met 595 600 605	1824
GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe 610 615 620	1872
ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe 625 630 635 640	1920
GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp 645 650 655	1968
AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp 660 665 670	2016

CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly 675 680 685	2064
CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly 690 695 700	2112
GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu 705 710 715 720	2160
TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp 725 730 735	2208
ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val 740 745 750	2256
GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe 755 760 765	2304
GTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 770 775 780	2352
GTC GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 785 790 795 800	2400
GTC GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA Leu Ala Leu Pro Pro Arg Ala Tyr Ala 805 810	2433

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr
180 185 190

Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro
210 215 220

Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val
225 230 235 240

Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr
245 250 255

Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
260 265 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser
275 280 285

Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
305 310 315 320

Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln
325 330 335

Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His
340 345 350

Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp
355 360 365

Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His
370 375 380

Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val
385 390 395 400

Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr
405 410 415

Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser
420 425 430

Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn
435 440 445

Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys
450 455 460

Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser
465 470 475 480

Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile
485 490 495

Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser
500 505 510

Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn
515 520 525

Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro
530 535 540

Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe
545 550 555 560

Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn
565 570 575

Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala
580 585 590

Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met
595 600 605

Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe
610 615 620

Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe
625 630 635 640

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
645 650 655

Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp
660 665 670

Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
675 680 685

Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
690 695 700

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu
705 710 715 720

Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp

725

730

735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
740 745 750

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe
755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
770 775 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu
785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala
805

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

1

5

10

15

Ser Pro Thr Thr Ala Leu
20

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
20 25 30

Pro Gly Cys Gly Lys
35

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr
1 5 10 15
Thr Ile Arg Arg His Val Asp Leu Leu
20 25

SEQUENCE DESCRIPTION

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
1 5 10 15
Ser Thr Gly Leu
20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro
1 5 10 15
Asn Ser Ser Ile
20

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile
1 5 10 15

Leu His Thr Pro
20

2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
1 5 10 15

Pro Gly Cys Val
20

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro
1 5 10 15
Thr Val Ala Thr
20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 5 10 15
Gln Leu Arg Arg
20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
1 5 10 15
Ala Thr Leu Cys
20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu
1 5 10 15
Cys Gly Ser Val
20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys
1 5 10 15
Asn Cys Ser Ile
20

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
1 5 10 15
Arg Met Ala Trp
20

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
1 5 10 15
Thr Ala Ala Leu
20

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
1 5 10 15
Pro Gln Ala Ile
20

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
1 5 10 15
Trp Gly Val Leu
20

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
1 5 10 15

Val Gly Asn Met
20

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser
1 5 10 15

Gly Gly Gln Ala
20

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln
1 5 10 15

Leu Ile Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser
1 5 10 15

Thr Ala Leu Asn
20

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu
1 5 10 15

Ile Tyr Gln His Lys
20

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu
1 5 10 15

Arg Leu Ala Ser
20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp
1 5 10 15

Gln Gly Trp Gly
20

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser
1 5 10 15

Gly Pro Asp Gln
20

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro
1 5 10 15

Pro Lys Pro Cys
20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val
1 5 10 15

Cys Gly Pro Val
20

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val
1 5 10 15

Val Val Gly Thr
20

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr
1 5 10 15

Tyr Ser Trp Gly
20

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val
1 5 10 15

Leu Asn Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

DRAFT
SEQUENCE
REPORT
TO DO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys
1 5 10 15

Val Cys Gly Ala
20

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala
1 5 10 15

Gly Asn Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Arg
1 5 10 15

Lys His Pro

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly
1 5 10 15

Ser Gly Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp
1 5 10 15

Tyr Pro Tyr Arg
20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

1

5

10

15

Asn Tyr Thr Ile
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly
1 5 10 15
Gly Val Glu His
20

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp
1 5 10 15
Thr Pro Gly Glu
20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp
1 5 10 15

Arg Ser Glu Leu
20

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr
1 5 10 15
Gln Trp Gln Val
20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCAGTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG 60

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAAC TGCATGATG 19

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

□ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCTCCATTGT GTATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GCCATACGCT CACAGCCGAT CCC

23